

Genetic Structure and Relationships among Populations of the Caspian Bent-toed Gecko, *Tenuidactylus caspius* (Eichwald, 1831) (Sauria: Gekkonidae) in Northern Iran

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Abstract The Caspian bent-toed gecko, *Tenuidactylus caspius*, belonging to the family Gekkonidae, is widely distributed across the northern half of Iran, especially along the southern coastal region of the Caspian Sea. It is regarded as a commensal species throughout its entire distribution. We investigated genetic variation and relationships among different populations of this species in Iran. Fragments of the mitochondrial *cyt b* (547 bp) and ND4 (831 bp) genes were sequenced and analyzed in 64 and 28 specimens, respectively, from 21 geographically distant localities. *Cyrtopodion scabrum* was used as the outgroup taxon. The data showed no significant genetic variation within the populations of *T. caspius* in Iran. Nevertheless, populations of Khorasan and Semnan (especially Shahrood) in northeastern Iran showed greater divergence (p -distance = 2.1%) from other Iranian populations. The low genetic variation and homogeneous structure among populations of *T. caspius* on either side of the Elburz Mountains suggests that this species most likely has achieved its current distribution recently and as a result of anthropogenic activities.

Keywords mtDNA, *Tenuidactylus caspius*, Gekkonidae, phylogeny, homogeneity, Iranian Plateau.

1. Introduction

The genus *Tenuidactylus* comprises seven species, three of which occur in Iran, chiefly in the eastern and northern portions of the country (Bauer *et al.*, 2013). *Tenuidactylus caspius* (Eichwald, 1831) is the most common gecko in northern Iran and comprises two subspecies in the Caspian Sea region (Leviton *et al.*, 1992; Szczerbak and Golubev, 1996; Anderson, 1999). *T. caspius caspius* is widely distributed in the eastern part of the Caucasus and Central Asia (Szczerbak, 2003; Kami, 2005). *T. caspius insularis* (Akhmedov and Szczerbak, 1978) occurs on the island of Vulf in the Caspian Sea and is known only from the type locality. It differs from the nominate subspecies

in having the first pair of postmental shields usually separated from each other by gular scales, although they may contact one another at a point, whereas in the nominate subspecies they are in broad contact (Akhmedov and Szczerbak, 1978).

In Iran *Tenuidactylus caspius* occurs in the northern part of the Iranian Plateau, an area affected by geological events in the Miocene (7-15 Million years ago). In particular, the uplift of the Elburz Mountains as well as the Kopet Dag and Caucasus regions has strongly influenced the diversity and evolution of reptiles in the area (Rastegar-Pouyani *et al.*, 2012). Leviton and Anderson (1984) indicated that divergence in the genus *Tenuidactylus* had started in the early Miocene (16-23 Millions of years ago, Ma). Bauer *et al.* (2013) suggested that the split between *T. caspius* plus *T. fedtschenkoi* and the other species of the genus had occurred 12 (7-17) Ma as a vicariant speciation event due to orogenic

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events in Iran and the Transcaspiian region. The process of diversification in *Tenuidactylus* may be comparable to that in the genus *Teratoscincus*, which had also been diversified in Central Asia (Macey *et al.*, 2005). Non-monophyly of the genus *Cyrtopodion sensu lato* has been demonstrated in several studies (Macey *et al.*, 2000; Gamble *et al.*, 2012) and the genus *Tenuidactylus* is considered as sister to a large clade including, *Agamura*, *Crossobamon*, *Bunopus* and *Cyrtopodion* (Bauer *et al.*, 2013).

Ahmadzadeh *et al.* (2010) examined morphological variation among populations of *T. caspius* in Iran, especially between the Moghan and Damghan populations. They clarified the presence of inter-population variation in most characters with particular emphasis of larger body size in Moghan specimens than in Damghan specimens. In a more recent study, however, no morphological differences (metric or meristic) were found among populations of this species from across all parts of northern Iran (Hojati, 2012).

Intraspecific differentiation of a species is usually attributed to geographic, demographic, and ecological factors that have operated throughout its evolutionary history (Walker and Avise, 1998). This may be particularly apparent in taxa that show only limited mobility, such as reptiles, while commensal geckos can easily be transported into new regions by anthropogenic means (e.g., *Hemidactylus turcicus* in the USA: Davis,

1974; Kraus, 2009). Molecular markers are of great value to study intraspecific variation and its geographic association, and to infer the evolutionary history of a species, especially in cases of phenotypic variation (Moritz and Hillis, 1996; Cruzan and Templeton, 2000).

We therefore addressed the question of intraspecific differentiation in *T. caspius* by inferring a molecular phylogeny using mitochondrial cytochrome b (cyt *b*) and ND4 gene sequences. These markers have proven to be very useful in various investigations of molecular phylogeography and systematics in reptiles (e.g., Wink *et al.*, 2001; Guicking *et al.*, 2002a, b; Nagy *et al.*, 2002; Carranza *et al.*, 2004; Carranza and Arnold, 2006; Carranza and Arnold, 2012; Kindler *et al.*, 2013).

2. Materials and Methods

2.1 Sampling A total of 64 specimens of *Tenuidactylus caspius* were collected between 2011 and 2012 from 21 geographically distant localities covering all parts of the species' distributional range in Iran (Figure 1). Tissue samples were preserved in absolute ethanol and were deposited in the Sabzevar University Herpetological Collection (SHUC). Based on the present knowledge of the phylogenetic relationships among *Tenuidactylus* and its allied genera, *Cyrtopodion scabrum* was chosen as an outgroup taxon. The complete list of materials examined and their GenBank accession numbers are given in Appendix 1 and 2.

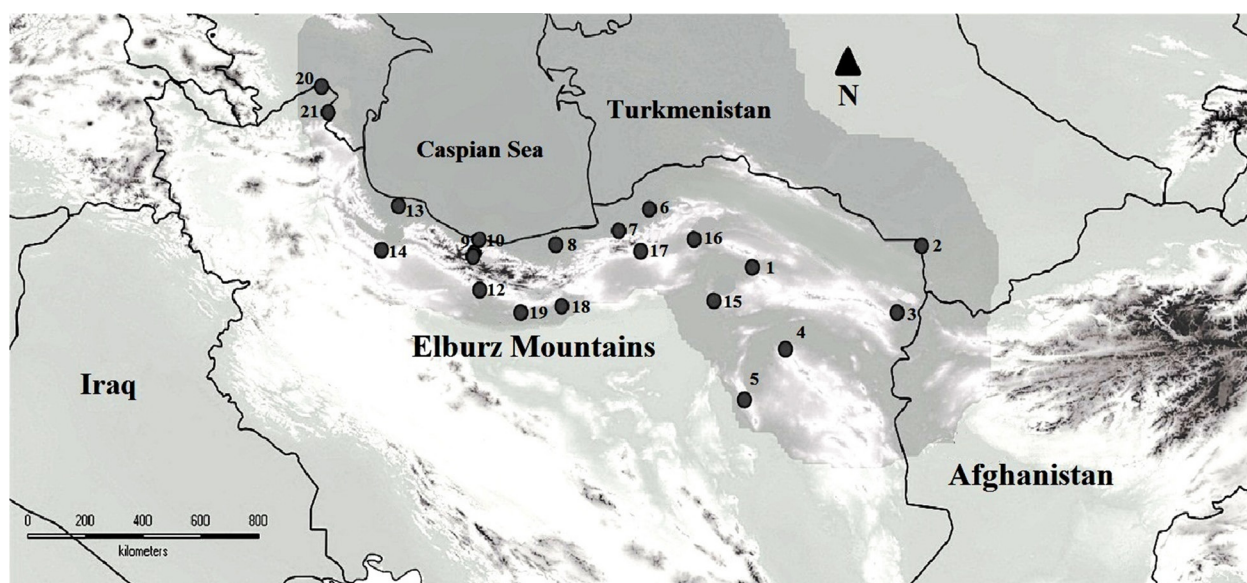


Figure 1 Map of Iran and adjacent countries, showing distribution of *Tenuidactylus caspius* and localities in which samples for this study were collected. Numbers in blue circles indicate the location number.

2.2 DNA extraction and PCR amplification Genomic DNA from each muscle and liver tissue sample was extracted using the salt method (Kabir *et al.*, 2006). Fragments of the mitochondrial cytochrome *b* (cyt *b*) and NADH Dehydrogenase subunit 4 (ND4) genes were amplified with the primers Mta_new and Ei700r (Rastegar-Pouyani *et al.*, 2010) and ND4 and Leu (Arévalo *et al.*, 1994), respectively. Relevant programs for PCR were extracted from following references (Arévalo *et al.*, 1994; Rastegar-Pouyani *et al.*, 2010) and were slightly modified for use in *Tenuidactylus*.

2.3 Phylogenetic analyses DNA sequences of 547 bp of cyt *b* and 831 bp of ND4 were aligned using BioEdit 7.0 (Hall, 1999) with default parameters. As both of the genes sequenced are protein coding, nucleotide sequences revealed were translated into amino acid sequences to evaluate the presence of inspected stop codons (none were detected). To perform ML and Bayesian analyses, the best-fitting evolutionary model was chosen for our dataset using jModelTest 2.1.1 (Posada, 2008), under corrected Akaike Information Criterion (AICc) and Bayesian Information Criterion (BIC).

Three methods of phylogenetic analyses were performed: Maximum Likelihood (ML), Maximum Parsimony (MP) and Bayesian Inference (BI). Based on the present knowledge of phylogenetic relationships among gekkotan lizards, sequences of *Cyrtopodion scabrum*, retrieved from the GenBank, were selected as the outgroup taxon. ML was conducted using the selected 27 sequences as a combined data set of cyt *b* and ND4 with the program RaxML ver. 7.0.3 (Stamatakis, 2006) under GTRGAMMA model with 1000 bootstrap replicates. In this analysis, *Tropiocolotes steudneri* was chosen as the outgroup taxon due to its close affinity to *Tenuidactylus* (Bauer *et al.*, 2013), and GenBank sequence availability for both genes of interest. Maximum Parsimony analyses were performed in PAUP*4.0 (Swofford, 2003) with all sites weighted equally; saturation effects were negligible in our data set. A Bayesian analysis was carried out using Mr.Bayes 3.1.2 (Huelsenbeck and Ronquist, 2001). A partitioned Bayesian analysis was performed in four chains and two independent runs for four million generations with model parameters for each gene partition (GTR + I + G for both cyt *b* and ND4). This model was obtained using the program jModelTest with AICc criterion. The analyses were started with randomly generated trees and every 100th tree was sampled. The log-likelihood of the 100000 trees in each analysis was plotted against the generation time. After verifying that saturation had been reached,

both in the term of likelihood scores and parameter estimation, the first 25% of trees were discarded in both runs, and a majority-rule consensus tree was generated from the remaining 75% (postburnin) trees. The frequency of any particular clade among the individual trees contributing to the consensus tree represents the posterior probability of that clade (Huelsenbeck and Ronquist, 2001). Average uncorrected genetic distances (*p*-distance) between groups of *T. caspius* were calculated in MEGA 5.1 (Tamura *et al.*, 2011). Combined sequences of cyt *b* and ND4 for 27 samples were employed to create haplotype network. For this purpose, sequences inserted to the software PHASE v. 2.1.1 that implemented in DNAsp (Librado and Rozas, 2009) for resolving phased haplotypes (Stephens *et al.*, 2001). Haplotype network were done using Network v. 4.5.1.0 (Bandelt *et al.*, 1999) with median joining option and default setting.

3. Results

Our *Tenuidactylus caspius* dataset of aligned sequences consisted of 547 bp of cytochrome *b* for 64 specimens and 831 bp of ND4 for 28 individuals. The best fit model of sequence evolution was GTR+G+I for cyt *b*; GTR+G for ND4 and HKY +G model for the combined dataset. Results from the three methods of phylogenetic analyses, to the great extent, supported the similar tree topology for both genes, either for individual gene trees or in the trees recovered from the combined dataset. BI tree for cyt *b* and ML tree for the combined dataset are presented in Figures 2 and 3, respectively. Due to extensive non-overlap of samples for the two genes, we did not concatenate our data for all samples included in the study. Two major clades can be defined within the phylogenetic trees, North/northwest and East/northeast clades. Clade separation is relatively well supported (91% of bootstrap value) in the cyt *b* tree. In addition, within the East/northeast clade, populations of Khorasan Province (Sabzevar, Bejestan, Sarakhs, Torbat Jam, boshrouyeh and Gonabad) and Semnan (especially Shahrood) populations were clearly differentiated from each other. The North/northwest clade is a quite heterogeneous clade with several subclades, however the amounts of genetic divergence among the subclades are relatively small. In general, all inter-population divergences within the local populations of this species in Iran are small (Table 1); 1.2% to 2% among the clades. Haplotype network were provided for 27 combined sequences of cyt *b* and ND4 (Figure 4) and as it is clear, northern and northwestern populations are divided from Semnan and eastern

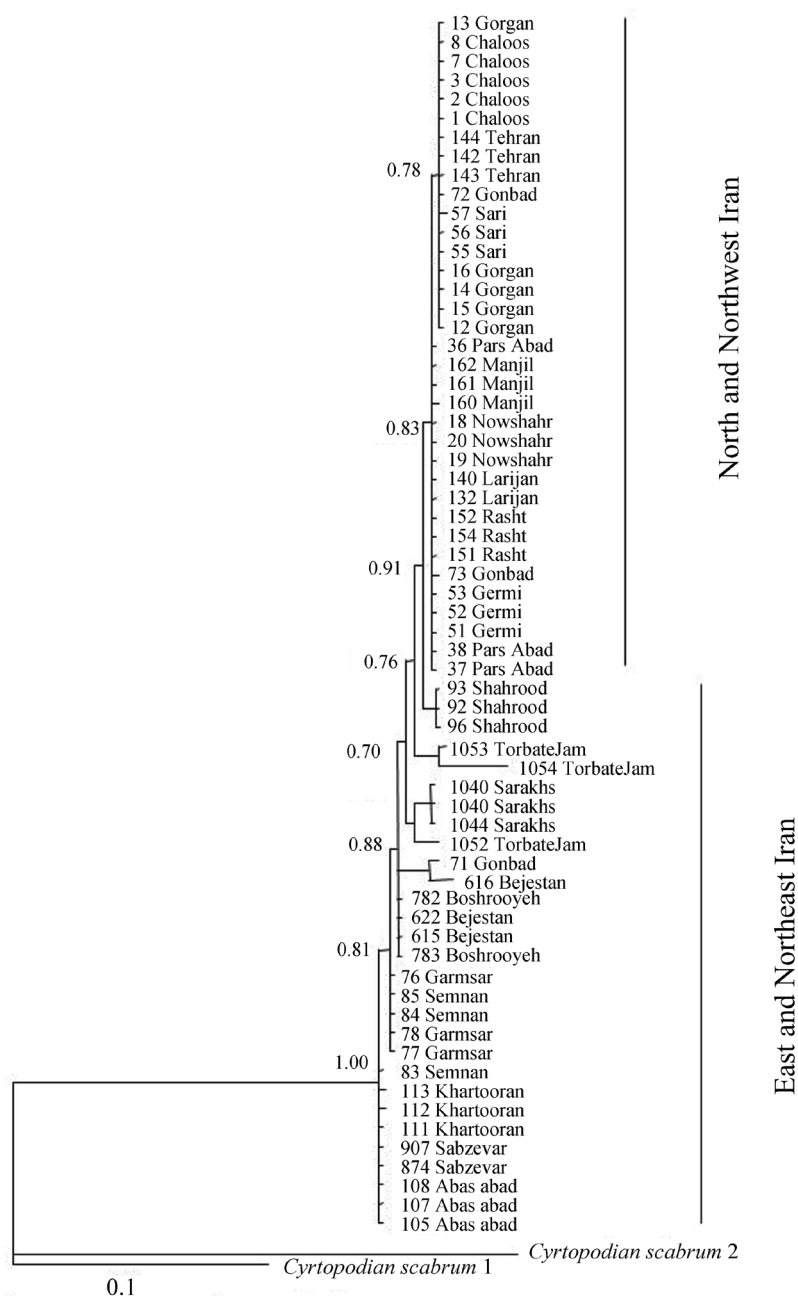


Figure 2 Phylogenetic relationships among the *T. caspius* populations included in the analysis. Individuals of *C. scabrum* were used as outgroups. Only the BI tree of cyt *b* is presented. Numbers close to the branches are posterior probabilities.

populations (Khorasan). Haplotype diversity estimated as 0.9516. Having 16 different haplotypes within the vast range of this species in Iran possibly indicates a relatively recent dispersal and diversification of the clade in the area a whole.

The highest genetic diversity (*p*-distance) of cyt *b* between populations was 2%, between the Shahrood (clade 4) and Khorasan populations (clade 5) (Figure2).

The lower divergence value was 1.2% between North + Tehran and Shahrood populations (clades 2 and 4, respectively).

As shown in Table 1, the *T. caspius* populations, based on sequencing of cyt *b* gene, have much larger cyt *b* *p*-distances of 23.5% to 24.6% with outgroup taxon.

Genetic distances for ND4 sequences (28 specimens) show a high similarity between Khartooran and Semnan

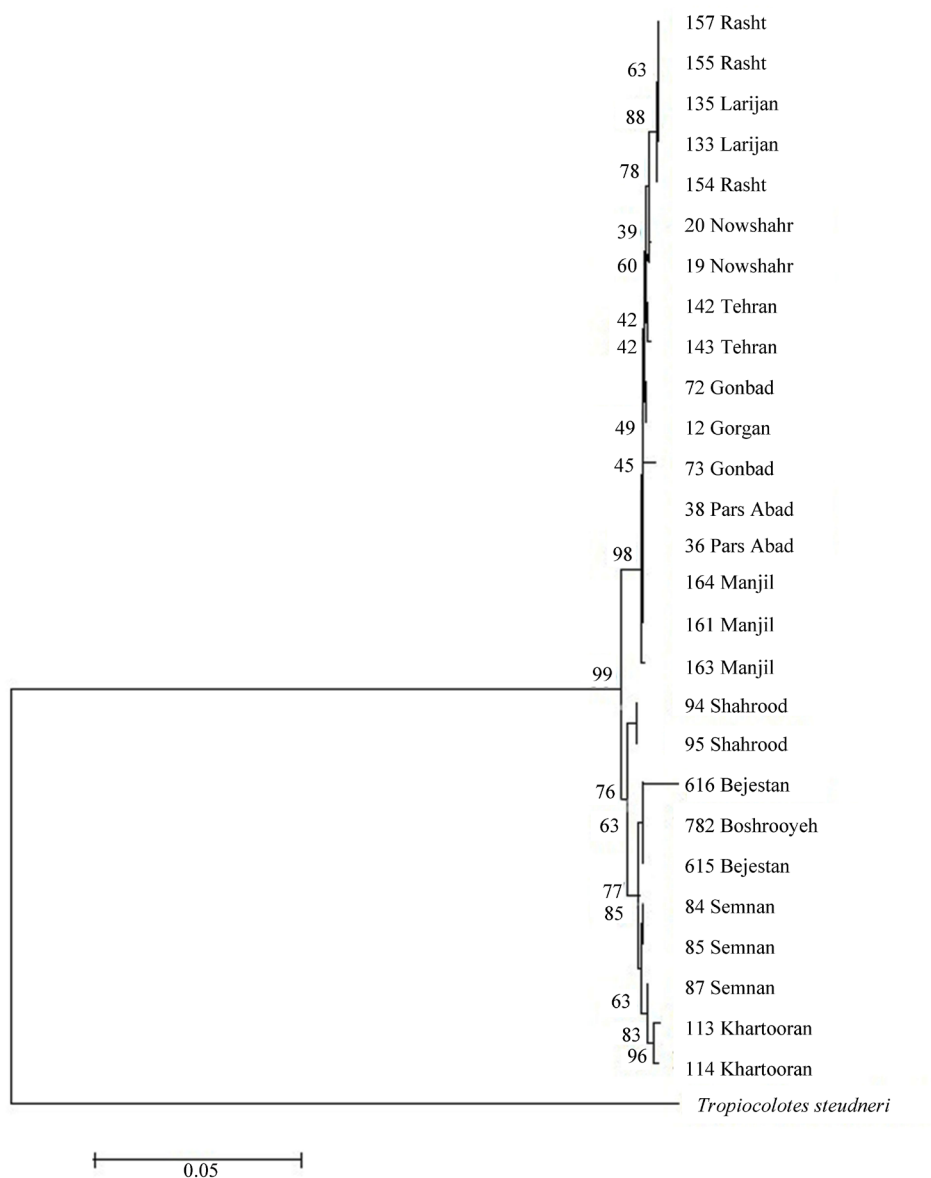


Figure 3 ML analysis of the phylogenetic relationships among populations of *T. caspius* based on 1378 bp of *cyt b* and ND4 sequences. Numbers close to the nodes are bootstrap supports with 2000 replicates.

Table 1 Genetic distances (*p*-distance) between major clades of the *T. caspius* complex included in this study (*Cyt b*).

	[1]	[2]	[3]	[4]	[5]
[1]					
[2]	0.244				
[3]	0.235	0.013			
[4]	0.246	0.012	0.015		
[5]	0.242	0.019	0.016	0.02	

[1] = Outgroup, [2] = North + Tehran, [3] = Semnan+Khartooran, [4] = Shahrood, [5] = Khorasan.

populations and a divergence of approximately 2% from all other clades. Both markers suggest that the species does not exhibit clear divergence among its Iranian populations; rather there is only a low variation (2%) between eastern and north-northwestern clades.

4. Discussion

Geographic genetic variation among conspecific populations is usually affected by both ecological and natural factors. Species adaptation and tolerance in different habitats are highly related to the ecological

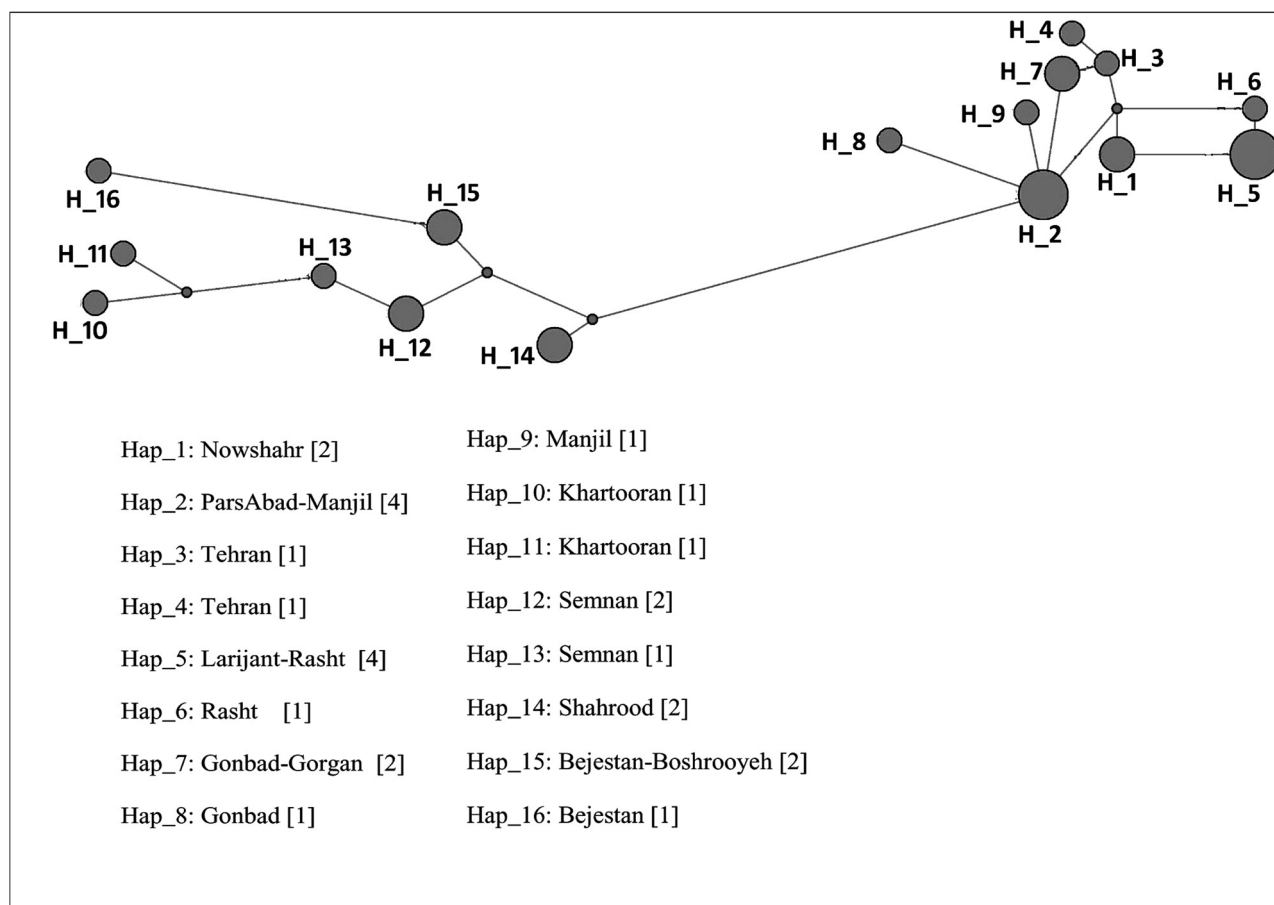


Figure 4 Parsimony network related to *cyt b* and ND4 sequences. Lines represent a mutational step, circles haplotypes and dots unsampled haplotypes. The size of circles is proportional to the number of individuals. Numbers next to the circles represent the haplotype localities as shown in the bottom of figure separately.

factors of the habitats that species can dwell but natural factors are related to population's dynamics and dispersal waves and vicariance events (Riddly, 2004). Samples used in this study were collected from throughout the area of the species' distribution in Iran (Figure 1) and neither of the mitochondrial genes showed significant differences among populations, indicating a homogeneous genetic structure within the species populations in a vast area of distribution rang in Iran. There are several polytomies in the both individual and combined trees, (Figures 2 and 3) this also in turn indicates that either the populations of *T. caspius* are still not genetically diverged properly or markers used in the study are not sufficient enough to reveal real divergence among the clades. However, a massive body of recent molecular studies indicated that the markers used in this study are quite adequate for revealing genetic divergence among populations of a species (e.g., Heidari *et al.*, 2011). A comparable study on another widespread gecko in Iran, *Cyrtopodion scabrum*, using sequences of *cyt b* shows the similar results (Fili,

2012).

Several comprehensive studies have been done to estimate the phylogenetic relationships among geckos. Nazarov and Poyarkov (2013) performed a project on the genus *Cyrtopodin* using a mitochondrial gene (COI), which resulted in recognition of an undescribed species of this genus in Uzbekistan.

Based on previous molecular studies, *T. caspius* was identified as an extant but old species (Bauer *et al.*, 2013). This species is estimated to have diverged from the closely related *T. fedtschenkoi* about 12 Ma when the Kopet Dagh was not yet raised and the Elburz Mountains had started to uplift (Alaeei, 2009).

Hojati (2012) studied *Tenuidactylus caspius* morphologically and found no significant differences across northern Iran. In contrast, however, Ahmadzadeh *et al.* (2010) argued that this species is morphologically relatively variable in Iran. On the other hand, Oraei (2009) and Fili (2012) showed high genetic and morphologic homogeneity in all populations of

Cyrtopodion scabrum in Iran and Hojati (2012) also presented a similar result for *T. caspius*. The main finding of this study is that despite its vast distribution area with many local populations, *T. caspius* is a homogeneous clade and there are no significant genetic differences among geographically distant populations.

Genetic variation among the Iranian populations of *Tenuidactylus caspius* is low and the genetic structure of this species is relatively homogeneous. Our data show that despite the presence of a vast geographic barrier (the Elburz Mountains), the genetic distance between Tehran and North Iran populations (12 for Tehran and 9-10-11 for north group in Figure 1) are very low. It appears that anthropogenic activities may be responsible for the recent dispersal of this species in the area as a similar situation has been documented for *Cyrtopodion scabrum* in Iran (Fili, 2012). *T. caspius* can be found around humans and is known as a commensal species in northern Iran. Such movements by humans swamp out the effects of natural barriers and historical biogeography on patterns of variation.

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Appendix 1 List of samples of *Tenuidactylus caspius* with their geographical origin and relevant accession number in GeneBank.

Museum number	Species	Locality; number in Figure 1	Latitude (N) °	Longitude (E) °	Accession numbers
					Cyt <i>b</i>
874	<i>Tenuidactylus caspius</i>	Sabzevar-1	31.12	57.43	KJ486228
907	<i>Tenuidactylus caspius</i>	Sabzevar-1	31.12	57.43	KJ486229
1040	<i>Tenuidactylus caspius</i>	Sarakhs-2	36.53	61.16	KJ486225
1039	<i>Tenuidactylus caspius</i>	Sarakhs-2	36.53	61.16	KJ486226
1044	<i>Tenuidactylus caspius</i>	Sarakhs-2	36.53	61.16	KJ486227
1052	<i>Tenuidactylus caspius</i>	Torbate Jam-3	35.24	60.62	KJ486222
1053	<i>Tenuidactylus caspius</i>	Torbate Jam-3	35.24	60.62	KJ486223
1054	<i>Tenuidactylus caspius</i>	Torbate Jam-3	35.24	60.62	KJ486224
615	<i>Tenuidactylus caspius</i>	Bejestan-4	34.51	58.17	KJ486232
616	<i>Tenuidactylus caspius</i>	Bejestan-4	34.51	58.17	KJ486233
622	<i>Tenuidactylus caspius</i>	Bejestan-4	34.51	58.17	KJ486234
782	<i>Tenuidactylus caspius</i>	Boshrooyeh-5	33.52	57.27	KJ486230
783	<i>Tenuidactylus caspius</i>	Boshrooyeh-5	33.52	57.27	KJ486231
71	<i>Tenuidactylus caspius</i>	Gonbad-6	37.25	55.17	KJ486193
72	<i>Tenuidactylus caspius</i>	Gonbad-6	37.25	55.17	KJ486194
73	<i>Tenuidactylus caspius</i>	Gonbad-6	37.25	55.17	KJ486195
13	<i>Tenuidactylus caspius</i>	Gorgan-7	36.83	54.48	KJ486179
12	<i>Tenuidactylus caspius</i>	Gorgan-7	36.83	54.48	KJ486180
15	<i>Tenuidactylus caspius</i>	Gorgan-7	36.83	54.48	KJ486181
14	<i>Tenuidactylus caspius</i>	Gorgan-7	36.83	54.48	KJ486182
16	<i>Tenuidactylus caspius</i>	Gorgan-7	36.83	54.48	KJ486183
55	<i>Tenuidactylus caspius</i>	Sari-8	36.55	53.1	KJ486190
56	<i>Tenuidactylus caspius</i>	Sari-8	36.55	53.1	KJ486191
57	<i>Tenuidactylus caspius</i>	Sari-8	36.55	53.1	KJ486192
19	<i>Tenuidactylus caspius</i>	Nowshahr-9	36.39	51.29	KJ486216
20	<i>Tenuidactylus caspius</i>	Nowshahr-9	36.39	51.29	KJ486217
18	<i>Tenuidactylus caspius</i>	Nowshahr-9	36.39	51.29	KJ486218
1	<i>Tenuidactylus caspius</i>	Chaloos-10	36.66	51.41	KJ486235
2	<i>Tenuidactylus caspius</i>	Chaloos-10	36.66	51.41	KJ486236
3	<i>Tenuidactylus caspius</i>	Chaloos-10	36.66	51.41	KJ486237
7	<i>Tenuidactylus caspius</i>	Chaloos-10	36.66	51.41	KJ486238
8	<i>Tenuidactylus caspius</i>	Chaloos-10	36.66	51.41	KJ486239
132	<i>Tenuidactylus caspius</i>	Larijan-11	36.06	52.15	KJ486214
140	<i>Tenuidactylus caspius</i>	Larijan-11	36.06	52.15	KJ486215
143	<i>Tenuidactylus caspius</i>	Tehran-12	35.67	51.42	KJ486208
142	<i>Tenuidactylus caspius</i>	Tehran-12	35.67	51.42	KJ486209
144	<i>Tenuidactylus caspius</i>	Tehran-12	35.67	51.42	KJ486210
151	<i>Tenuidactylus caspius</i>	Rasht-13	37.3	49.63	KJ486211
154	<i>Tenuidactylus caspius</i>	Rasht-13	37.3	49.63	KJ486212
152	<i>Tenuidactylus caspius</i>	Rasht-13	37.3	49.63	KJ486213
160	<i>Tenuidactylus caspius</i>	Manjil-14	36.44	49.25	KJ486219
161	<i>Tenuidactylus caspius</i>	Manjil-14	36.44	49.25	KJ486220
162	<i>Tenuidactylus caspius</i>	Manjil-14	36.44	49.25	KJ486221
111	<i>Tenuidactylus caspius</i>	Khartooran-15	35.47	56.6	KJ486240
112	<i>Tenuidactylus caspius</i>	Khartooran-15	35.47	56.6	KJ486241
113	<i>Tenuidactylus caspius</i>	Khartooran-15	35.47	56.6	KJ486242
105	<i>Tenuidactylus caspius</i>	Abbas Abad-16	36.33	51.28	KJ486205
107	<i>Tenuidactylus caspius</i>	Abbas Abad-16	36.33	51.28	KJ486206
108	<i>Tenuidactylus caspius</i>	Abbas Abad-16	36.33	51.28	KJ486207
93	<i>Tenuidactylus caspius</i>	Shahrood-17	36.42	54.97	KJ486202
96	<i>Tenuidactylus caspius</i>	Shahrood-17	36.42	54.97	KJ486203
92	<i>Tenuidactylus caspius</i>	Shahrood-17	36.42	54.97	KJ486204
83	<i>Tenuidactylus caspius</i>	Semnan-18	35.35	53.23	KJ486199
84	<i>Tenuidactylus caspius</i>	Semnan-18	35.35	53.23	KJ486200
85	<i>Tenuidactylus caspius</i>	Semnan-18	35.35	53.23	KJ486201
76	<i>Tenuidactylus caspius</i>	Garmsar-19	35.22	52.33	KJ486196
77	<i>Tenuidactylus caspius</i>	Garmsar-19	35.22	52.33	KJ486197
78	<i>Tenuidactylus caspius</i>	Garmsar-19	35.22	52.33	KJ486198
36	<i>Tenuidactylus caspius</i>	Pars Abad-20	39.65	47.93	KJ486184
37	<i>Tenuidactylus caspius</i>	Pars Abad-20	39.65	47.93	KJ486185
38	<i>Tenuidactylus caspius</i>	Pars Abad-20	39.65	47.93	KJ486186
51	<i>Tenuidactylus caspius</i>	Germi-21	39.13	48.08	KJ486187
52	<i>Tenuidactylus caspius</i>	Germi-21	39.13	48.08	KJ486188
53	<i>Tenuidactylus caspius</i>	Germi-21	39.13	48.08	KJ486189

Appendix 2 ND4 accession numbers (28 samples).

species	locality	Latitude (N) °	Longitude (E) °	Accession Number
<i>Tenuidactylus caspius</i>	20-Nowshahr	36.39	51.29	KJ486243
<i>Tenuidactylus caspius</i>	19-Nowshahr	36.39	51.29	KJ486244
<i>Tenuidactylus caspius</i>	25-Amol	36.23	52.20	KJ486245
<i>Tenuidactylus caspius</i>	28-Amol	36.23	52.20	KJ486246
<i>Tenuidactylus caspius</i>	38-Pars Abad	39.65	47.93	KJ486247
<i>Tenuidactylus caspius</i>	36-Pars Abad	39.65	47.93	KJ486248
<i>Tenuidactylus caspius</i>	122-Galogah	36.82	53.87	KJ486249
<i>Tenuidactylus caspius</i>	142-Tehran	35.67	51.42	KJ486250
<i>Tenuidactylus caspius</i>	143-Tehran	35.67	51.42	KJ486251
<i>Tenuidactylus caspius</i>	133-Larijan	36 06	52 15	KJ486252
<i>Tenuidactylus caspius</i>	135-Larijan	36 06	52 15	KJ486253
<i>Tenuidactylus caspius</i>	157-Rasht	37.30	49.63	KJ486254
<i>Tenuidactylus caspius</i>	155-Rasht	37.30	49.63	KJ486255
<i>Tenuidactylus caspius</i>	154-Rasht	37.30	49.63	KJ486256
<i>Tenuidactylus caspius</i>	163-Manjil	36.44	49.25	KJ486257
<i>Tenuidactylus caspius</i>	164-Manjil	36.44	49.25	KJ486258
<i>Tenuidactylus caspius</i>	161-Manjil	36.44	49.25	KJ486259
<i>Tenuidactylus caspius</i>	12-Gorgan	36.83	54.48	KJ486260
<i>Tenuidactylus caspius</i>	113-Khartooran	35.47	56.60	KJ486261
<i>Tenuidactylus caspius</i>	114-Khartooran	35.47	56.60	KJ486262
<i>Tenuidactylus caspius</i>	84-Semnan	35.35	53.23	KJ486263
<i>Tenuidactylus caspius</i>	85-Semnan	35.35	53.23	KJ486264
<i>Tenuidactylus caspius</i>	87-Semnan	35.35	53.23	KJ486265
<i>Tenuidactylus caspius</i>	94-Shahrood	36.42	54.97	KJ486266
<i>Tenuidactylus caspius</i>	95-Shahrood	36.42	54.97	KJ486267
<i>Tenuidactylus caspius</i>	615-Bejestan	34.51	58.17	KJ486268
<i>Tenuidactylus caspius</i>	616-Bejestan	34.51	58.17	KJ486269
<i>Tenuidactylus caspius</i>	782-Boshrooyeh	33.52	57.27	KJ486270